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Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu 85 90 95

Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu Thr Met Glu 100 105 110

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Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Lys 195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu 210 220

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Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser 695 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu Leu Arg Arg Gln Lys 755 <210> 24 <211> 5169 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: WSN-PB1 <220> <221> CDS <222> (191)..(2461) <400> 24 cccaaaaaaa aaaaaaaaa aagagtccag agtggcccg ccgctccgcg ccgggggggg 60 ggggggggg ggacactttc ggacatctgg tcgacctcca gcatcggggg aaaaaaaaa 120 acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180 aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro 20 tac age cat ggg aca gga aca gga tac ace atg gat act gte aac agg 325 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg 30 40 aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421 Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469 Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517 Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu 100 acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565 Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly 110 115 120

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ij.

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709

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520

Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala 535 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser 585 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu 600 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu 615 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg Ser Ile Leu Asn Thr Ser Gin Arg Gly Ile Leu Glu Asp Glu Gln Met 680 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser 705 710 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys

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cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile 190 195 200	
ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala 210 215 220	
tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys 225 230 235	
cgg aga gca att gca aca cca ggg atg cag atc aga ggg ttt gtg tac Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr 240 245 250	
ttt gtt gag aca ctg gcg aga agc att tgc gag aag ctt gaa cag tct Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser 255 260 265	

						aat Asn										1045
						aac Asn										1093
						aaa Lys										1141
						tac Tyr										1189
						gcg Ala 340										1237
						atg Met										1285
						atg Met										1333
					_	aaa Lys										1381
						agc Ser										1429
atg Met	ctg Leu 415	agt Ser	aca Thr	gtg Val	ttg Leu	gga Gly 420	gtc Val	tca Ser	atc Ile	ctg Leu	aat Asn 425	ctt Leu	Gl A āāā	caa Gln	aag Lys	1477
						tac Tyr										1525
_						aat Asn										1573
						aga Arg										1621
						ata Ile										1669
agc Ser	ttt Phe 495	ttc Phe	tac Tyr	cgc Arg	tat Tyr	gga Gly 500	ttt Phe	gta Val	gcc Ala	aat Asn	ttt Phe 505	agt Ser	atg Met	gag Glu	ttg Leu	1717
						gga Gly										1765

					aag Lys											1813
					gct Ala											1861
					agg Arg											1909
					ctg Leu											195-
_	_		-		gga Gly 595			_								2005
					ctg Leu											2053
			_		ccc Pro	_				-	_		_	-		2101
					gct Ala											2149
					gct Ala											219-
_		_			ctc Leu 675		_	-							-	2245
					aag Lys											2293
_	-			-	aga Arg		_				-	_			-	2341
					cgg Arg											2389
					gag Glu											243
					cgg Arg 755			tagt	gaat	itt a	agctt	gtc	ct to	catga	aaaa	2491
atg	cctt	gtt t	ctac	ctaat	a ac	ccgg	gegge	cca	aaaat	gcc	gact	cgga	agc (gaaaq	gatata	2551
cct	cccc	egg g	ggcc	ggga	gg to	egegt	caco	gad	ccacç	gccg	ccg	gecea	agg (cgac	gcgcga	2611
cac	ggaca	acc t	gtco	ccaa	aa aa	cgcc	cacca	tcg	gcago	ccac	acad	cggaq	gcg (cccg	gagccc	2671
tct	ggtca	ac c	ccaç	ggaca	ac ac	gege	gago	ago	gccç	lggc	cgg	ggacq	gcc (ctac	cāāccā	2731

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tagaaaaata aacaaaagag tttgtagaaa cgcaaaaagg ccatccgtca ggatggcctt 4771 ctgcttaatt tgatgcctgg cagtttatgg cgggcgtcct gcccgccacc ctccgggccg 4831 ttgcttcgca acgttcaaat ccgctcccgg cggatttgtc ctactcagga gagcgttcac 4891 cgacaaacaa cagataaaac gaaaggccca gtctttcgac tgagcctttc gttttatttg 4951 atgcctggca gttccctact ctcgcatggg gagaccccac actaccatcg gcgctacggc 5011 gtttcacttc tgagttcggc atggggtcag gtgggaccac cgcgctactg ccgccaggca 5071 aattctgttt tatcagaccg cttctgcgtt ctgatttaat ctgtatcagg ctgaaaatct 5131 tctccatcc gccaaaacag ccaagctagc ggccgatc 5069

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<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pHL3130

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Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
20 25 30

Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln 35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro 50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu 85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu 100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Tnr 115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala 130 135 140

Asn Thr Ile Glu Val Fhe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser 145 150 155 160

Gly Arg Leu Ile Asp Fne Leu Lys Asp Val Met Glu Ser Met Asn Lys 165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg 180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg 195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu 210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu 250 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly 300 Asp Asn Thr Lys Trp Asn Glu Asn Gin Asn Pro Arg Met Phe Leu Ala Met lle Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val 325 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly 345 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile 360 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro 375 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn Met Leu Ser 405 410 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg Tyr Thr 425 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala Leu lle Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe 490 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe 505 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr 520 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala 535 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg 550 555 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu

570

Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser 585 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu 595 600 605 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val 630 635 Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser 695 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys 730 Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu Leu Arg Arg Gln Lys 755 <210> 32 <211> 5169 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: pHL3131 <220> <221> CDS <222> (191)..(2461) <400> 32 cccaaaaaaa aaaaaaaaa aagagtccag aqtqqccccg ccqctccqcq ccqqqqqqq 60 acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180 aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro gea caa aat get ata age aca act tte eet tat act gga gae eet eet 277 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro 15 tac age cat ggg aca gga aca gga tac ace atg gat act gtc aac agg Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg

				gaa Glu									373
	-	_		aac Asn	-		-		_		_	-	421
				gcc Ala									469
				cat His									517
				cag Gln 115									565
				tgg Trp									6 i 3
				ata Ile									661
	_		 	ctc Leu		_		_	_	_	_		709
				atg Met									757
				atg Met 195									805
				aga Arg									853
		_		atg Met			-	 	_		_		901
				aca Thr									949
				gcg Ala									997
				ggg Gly 275									1045
				acg Thr									1093

	acc Thr															1141
	ctg Leu		atg					aca					gag			1189
	aat Asn 335															1237
	cta Leu															1285
	caa Gln															1333
	gaa Glu															1381
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_	ctg Leu 415				_		_			_					_	1477
	tac Tyr															1525
	ttt Phe															1573
	gtg Val															1621
	aag Lys															1669
	ttt Phe 495															1717
	agc Ser										_	_	_	_		1765
	gtt Val		-					_				_				1813
_	acc Thr	_		_	-		_					_				1861
_	tac Tyr	-	_		_									_		1909

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ctg gtc tcc gac gga ggc cca aat tta tac aac att aga aat ctc cac 2 Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His 590 600 605	2005
att cct gaa gtc tgc ttg aaa tgg gaa tla atg gat gag gat tac cag 2 Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln 610 615 620	2053
ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att 2 Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile 625 630 635	2101
gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aaa 2 Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys 640 650	2149
aac atg gag tat gat gct gtt gca aca aca cac tcc tgg atc ccc aaa 2 Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys 655 660 665	21.97
aga aat cga tcc atc ttg aat aca agc caa aga gga ata ctt gaa gat 2 Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp 670 685	2245
gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc 2 Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro 690 695 700	2293
agc agt tca tac aga aga cca gtc ggg ata tcc agt atg gtg gag gct 2 Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala 705 710 715	2341
atg gtt tcc aga gcc cga att gat gca cga att gat ttc gaa tct gga 2 Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly 720 725 730	2389
agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc 2 Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr 735 740 745	2437
att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgtcct tcatgaaaaa 2 Ile Glu Glu Leu Arg Arg Gln Lys 750 755	2491
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<210> 33 <211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pHL3131

<400> 33

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Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His

Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln \$35\$

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro 50 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu 85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu 100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr 115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala 130 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser 145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys 165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg 180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg 195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu 210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala 225 230 235

Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu 245 250 255

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro 260 265 270

Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys 275 280 285 Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val 330 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly 345 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro 375 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn Met Leu Ser 410 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg Tyr Thr 425 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala 440 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe 490 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe 505 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr 520 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala 535 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg 555 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser 585 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val

Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu 645 650 655
Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg 660 665 670
Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met 675 680 685
Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser 690 695 700
Tyr Aig Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser 705 710 720
Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys 725 730 735
Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu 740 745 750
Leu Arg Arg Gln Lys 755
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acaaagtgte geeeggagta etggtegace teegaagttg ggggggageg aaageaggea 180
aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro 1 5 10
gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro 15 20 25
tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg 30 35 40 45
aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr 50 55 60
gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421 Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn 65 70 75
gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469

tte Phe	ctt Let 95	1 G11	g gaa 1 Gli	a tco u Sei	c cat	cct s Pro 100	o GT	t ato y Ile	c tti e Phe	t gaq e Gli	g aco u Thi 105	r Sei	g tgt Cys	ctt Leu	gaa Glu	517
acq Thi 11(. Met	g gaq : Gli	g gtt u Val	gtt L Val	caç Glr 115	ı Glr	a aca	a cga c Arg	g gto	g gad L Asp 120	D Lys	g cto s Lei	g aca ı Thr	caa Gln	ggc Gly 125	565
ega Arg	caç Glr	aco Thr	tat Tyr	gac Asp 130	Trp	act Thr	cta Leu	a aat 1 Asr	ago Aro 135	, Asr	caç n Glr	g cct n Pro	gct Ala	gca Ala 140	aca Thr	613
gca Ala	trg Leu	ged Ala	aac Asn 145	Thr	ata Ile	gaa Glu	gtg Val	tto Phe	Arg	tca Ser	a aat Asr	ggc Gly	ctc Leu 155	Thr	gcc Ala	661
aat Asn	gaa Glu	tct Ser 160	. GTA	agg Arg	ctc Leu	ata Ile	gac Asp 165	Phe	ctt Leu	aag Lys	g gat S Asp	gta Val 170	Met	gag Glu	tca Ser	709
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cgg Arg	aga Arg	gca Ala 240	att Ile	gca Ala	acc Thr	cca Pro	ggg Gly 245	atg Met	caa Gln	ata Ile	agg Arg	999 Gly 250	ttt Phe	gta Val	tac Tyr	949
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aga Arg	aat Asn 335	gtt Val	cta Leu	agt Ser	TIE.	gct Ala 340	cca Pro	ata Ile	atg Met	ttc Phe	tca Ser 345	aac Asn	aaa Lys	atg Met	gcg Ala	1237

aga Arq 350	J Let	g gga	a aaq y Lys	g ggg	g tac y Tyr 355	: Met	g ttt Phe	gaç Gli	g ago ı Sei	aaq Ly: 360	s Ser	ato Met	g aaa Lys	a att s Ile	aga Arg 365	1285
act Thr	caa Gln	ata Ile	a cct e Pro	gca Ala 370	ı Glu	ato Met	cta Leu	a gca a Ala	a ago a Ser 375	: Il ϵ	c gat e Asp	tto Leu	g aaa Lys	tac Tyr 380	ttc Phe	1333
aat Asn	gat Asp	tca Ser	act Thr 385	Arg	aag Lys	aag Lys	att Ile	gaa Glu 390	ı Lys	ato : Ile	c cgg e Arg	ccç Pro	cto Leu 395	ı Lev	ata Ile	1381
gat Asp	ggg Gly	act Thr 400	Ala	tca Ser	ttg Leu	agc Ser	cct Pro 405	Gly	atg Met	atç Met	g atg : Met	ggc Gly 410	Met	ttc Phe	aat Asn	1429
atg Met	tta Leu 415	Ser	act Thr	gta Val	tta Leu	ggc Gly 420	gtc Val	tcc Ser	atc	ctg Leu	aat Asn 425	ctt Leu	gga Gly	caa Gln	aag Lys	1477
aga Arg 430	cac His	acc Thr	aag Lys	act Thr	act Tnr 435	tac Tyr	tgg Trp	tgg Trp	gat Asp	ggt Gly 440	Leu	caa Gln	tct Ser	tct Ser	gat Asp 445	1525
gat Asp	ttt Phe	gct Ala	ctg Leu	att Ile 450	gtg Val	aat Asn	gca Ala	ccc Pro	aat Asn 455	cat His	gaa Glu	Gly	att Ile	caa Gln 460	gcc Ala	1573
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ccc Pro 510	agc Ser	ttt Phe	ggg Gly	gtg Val	tct Ser 515	Gl ^A aaa	atc Ile	aac Asn	gag Glu	tct Ser 520	gcg Ala	gac Asp	atg Met	agt Ser	att Ile 525	1765
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gaa Glu	tct Ser	gta Val 640	aac Asn	aat Asn	gct Ala	gcg Ala	gta Val 645	atg Met	cca Pro	gcc Ala	cat His	ggt Gly 650	cca Pro	gcc Ala	aaa Lys	2149
agc Ser	atg Met 655	gaa Glu	tat Tyr	gat Asp	gct Ala	gtg Val 660	gca Ala	act Thr	aca Thr	cac Hıs	tct Ser 665	tgg Trp	atc Ile	cct Pro	aag Lys	2137
670	Asn	Arg	Ser	lle	Leu 675	Asn	Thr	Ser	Gln	Arg 680	gga Gly	Ile	Leu	Glu	Asp 685	2245
GIU	GIN	Met	Tyr	GIn 690	Lys	Cys	Cys	Asn	Leu 695	Phe	gag Glu	Lys	Phe	Phe 700	Pro	2293
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															agtcc	
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<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pHL3203

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Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Asp Ser Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala 440 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys 475 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe 505 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser 585 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu 615 Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val 630 635 Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu 645 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser 695

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr 1le Glu Giu 745 Leu Arg Arg Gln Lys 755 <210> 36 <211> 5169 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: pHL3204 <220> <221> CDS <222> (191)..(2461) <400> 36 cccaaaaaaa aaaaaaaaa aagagtccag agtggccccg ccgctccgcg ccgggggggg 60 acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180 aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro 15 20 tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg 30 35 40 aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421 Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn 469 gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala 85 tto ott gag gaa too cat oot ggt ato ttt gag acc tog tgt ott gaa 517 Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu 100 acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565 Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly 110 115 120 cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr

						gaa Glu										661
						ata Ile										709
						gag Glu 180										757
						act Thr										805
			_	_	_	ttg Leu									_	853
						acc Thr		-	_	_	_		_			901
						cca Pro										949
	-				_	agg Arg 260			_				_			997
						aat Asn										1045
Gly 270 gta	Leu	Pro aag	Val atg	Gly	Gly 275 acc		Ğlu tot	Lys	Lys gac	Ala 280 act	Lys	Leu	Āla	Asn	Val 285 acc	1045
Gly 270 gta Val	Leu agg Arg	Pro aag Lys gga	Val atg Met gat	Gly atg Met 290 aac	Gly 275 acc Thr	Asn	Glu tct Ser	Lys cag Gln aac	Lys gac Asp 295	Ala 280 act Thr	Lys gaa Glu cag	Leu att Ile	Ala tct Ser	Asn ttc Phe 300	Val 285 acc Thr	
Gly 270 gta Val atc Ile	Leu agg Arg act Thr	Pro aag Lys gga Gly gcc	Val atg Met gat Asp 305 atg	Gly atg Met 290 aac Asn	Gly 275 acc Thr acc Thr	Asn aat Asn	Glu tct Ser tgg Trp	Lys cag Gln aac Asn 310 acc	Lys gac Asp 295 gaa Glu aga	Ala 280 act Thr aat Asn	Lys gaa Glu cag Gln	Leu att Ile aac Asn ccc	Ala tct Ser cct Pro 315 gaa	Asn ttc Phe 300 cgg Arg	Val 285 acc Thr atg Met	1093
Gly 270 gta Val atc Ile ttt Phe aga	Leu agg Arg act Thr ttg Leu aat	Pro aag Lys gga Gly gcc Ala 320 gtt	Val atg Met gat Asp 305 atg Met	Gly atg Met 290 aac Asn atc Ile	Gly 275 acc Thr acc Thr aca Thr	Asn aat Asn aaa Lys tat	Glu tct Ser tgg Trp ata Ile 325 cca	cag Gln aac Asn 310 acc Thr	gac Asp 295 gaa Glu aga Arg	Ala 280 act Thr aat Asn aat Asn	Lys gaa Glu cag Gln cag Gln	att Ile aac Asn ccc Pro 330 aac	Ala tct Ser cct Pro 315 gaa Glu aaa	Asn ttc Phe 300 cgg Arg tgg Trp	Val 285 acc Thr atg Met ttc Phe	1093
Gly 270 gta Val atc Ile ttt Phe aga Arg	Leu agg Arg act Thr ttg Leu aat Asn 335 ctg	Pro aag Lys gga Gly gcc Ala 320 gtt Val	Val atg Met gat Asp 305 atg Met cta Leu aag	atg Met 290 aac Asn atc Ile agt Ser	Gly 275 acc Thr acc Thr aca Thr att Ile	Asn aat Asn aaa Lys tat Tyr gct Ala	Glu tct Ser tgg Trp ata ile 325 cca Pro	Lys cag Gln aac Asn 310 acc Thr ata Ile	Lys gac Asp 295 gaa Glu aga Arg atg Met	Ala 280 act Thr aat Asn att Asn ttc Phe	Lys gaa Glu cag Gln cag Gln tca Ser 345	att Ile aac Asn ccc Pro 330 aac Asn	Ala tct Ser cct Pro 315 gaa Glu aaa Lys aaa	Asn ttc Phe 300 cgg Arg tgg Trp atg Met	Val 285 acc Thr atg Met ttc Phe gcg Ala	1093 1141 1189
Gly 270 gta Val atc Ile ttt Phe aga Arg asso act	agg Arg act Thr ttg Leu aat Asn 335 ctg Leu caa	Pro aag Lys gga Gly gcc Ala 320 gtt Val gga Gly ata	Val atg Met gat Asp 305 atg Met cta Leu aag Lys	atg Met 290 aac Asn atc Ile agt Ser ggg Gly	Gly 275 acc Thr acc Thr aca Thr att Ile tac Tyr 355 gaa	Asn aat Asn aaa Lys tat Tyr gct Ala 340 atg	Glu tct Ser tgg Trp ata Ile 325 cca Pro ttt Phe cta	cag Gln aac Asn 310 acc Thr ata Ile gag Glu gca	Lys gac Asp 295 gaa Glu aga Arg atg Met agc Ser	Ala 280 act Thr aat Asn aat Asn ttc Phe aag Lys 360 atc	Lys gaa Glu cag Gln cag Gln tca ser 345 agt Ser gat	att Ile aac Asn ccc Pro 330 aac Asn atg Met	Ala tct Ser cct Pro 315 gaa Glu aaa Lys aaa	Asn ttc Phe 300 cgg Arg tgg Trp atg Met att Ile tac	Val 285 acc Thr atg Met ttc Phe gcg Ala aga Arg 365 ttc	1093 1141 1189 1237

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						ggc Gly 420										1477
						tac Tyr										1525
_		_	_			aat Asn	_				_				_	1573
						cga Arg										1621
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						gga Gly										1765
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						gga Gly										1909
						tgg Trp 580										1957
						cca Pro										2005
		-	_	_	_	aaa Lys		-		_	-		-		_	2053
						ctg Leu										2101
						gtg Val										2149
						gtt Val 660										2197

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Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
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Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr 425 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe 505 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala 535 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu 615 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met 675 680 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser 695 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu 740 745 Leu Arg Arg Gln Lys 755

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gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 27 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro 15 20 25	7													
tac age cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 32 Tyr Ser His Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg 30 35 40 45	5													
aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 37 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr 50 55 60	3													
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gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc 66 Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala 145 150 155	1													
Eat gaa tot gga agg oto ata gao tto ott aag gat gta atg gag toa 70 Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser 160 165 170	9													
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							999 Gly 245									949
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							gtc Val									1477
							tgg Trp									1525
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Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro 50 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu 85 90 .95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu 100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr 115 120 125

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Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe 485 490 495

Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe 500 505 510

Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr 515 520 525

Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala 530 540

Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg 545. 550 560

Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile 565 570 575

Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser 580 590

Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu 595 600 605

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu 610 620

Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val 625 630 635 640

Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu 645 650 655

Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg 660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met 675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser 690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser 705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
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aaccatttga atg gat gtc aat ccg act Met Asp Val Asn Pro Thr 1 5	tta ctt ttc tta aaa gtg cca 229 Leu Leu Phe Leu Lys Val Pro 10
gca caa aat gct ata agc aca act tte Ala Gln Asn Ala Ile Ser Thr Thr Ph 15 20	c cct tat act gga gac cct cct 277 e Pro Tyr Thr Gly Asp Pro Pro 25
tac age cat ggg aca gga aca gga ta Tyr Ser His Gly Thr Gly Thr Gly Ty 30 35	
aca cat cag tac tca gaa agg gga ag Thr His Gln Tyr Ser Glu Arg Gly Ard 50	
gga gca ccg caa ctc aac ccg att ga Gly Ala Pro Gln Leu Asn Pro Ile As 65	p Gly Pro Leu Pro Glu Asp Asn
gaa cca agt ggt tat gcc caa aca ga Glu Pro Ser Gly Tyr Ala Gln Thr Asp 80 85	
ttc ctt gag gaa tcc cat cct ggt atc Phe Leu Glu Glu Ser His Pro Gly Ilo 95 100	
acg atg gag gtt gtt cag caa aca cga Thr Met Glu Val Val Gln Gln Thr Arc 110	
cga cag acc tat gac tgg act cta aad Arg Gln Thr Tyr Asp Trp Thr Leu Asi 130	
gca ttg gcc aac aca ata gaa gtg ttc Ala Leu Ala Asn Thr Ile Glu Val Pho 145	e Arg Ser Asn Gly Leu Thr Ala
aat gaa tot gga agg oto ata gao tto Asn Glu Ser Gly Arg Leu Ile Asp Pho 160 165	
atg aac aaa gaa gaa atg gag atc aca Met Asn Lys Glu Glu Met Glu Ile Th 175 180	
cga gtg aga gac aat atg act aag aa: Arg Val Arg Asp Asn Met Thr Lys Ly: 190 195	
ggt aaa agg aag cag aga ttg aac aaa Gly Lys Arg Lys Gln Arg Leu Asn Lys 210	
tta acc ctg aac aca atg acc aaa ga Leu Thr Leu Asn Thr Met Thr Lys Asp 225 230	o Ala Glu Arg Gly Lys Leu Lys

cg(Ar	g aga g Aro	a gca g Ala 240	a 1⊺€	gca Ala	a aco	cca Pro	ggg Gly 245	Met Met	g caa : Glr	a ata n Ile	a ago	g ggg g Gl ₃ 250	/ Phe	gta Val	a tac L Tyr	949
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aat Asn	gaa Glu	cca Pro	aca Thr 385	agg Arg	aag Lys	aaa Lys	atc Ile	gag Glu 390	aaa Lys	ata Ile	agg Arg	cct Pro	ctc Leu 395	ata Ile	ata Ile	1381
gac Asp	Gly	aca Thr 400	gcc Ala	tca Ser	tta Leu	agc Ser	ccg Pro 405	gga Gly	atg Met	atg Met	atg Met	ggt Gly 410	atg Met	ttc Phe	aac Asn	1429
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Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln 35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro 50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu 85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu 100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr 115 120

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala 130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser 145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys 165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly 295 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala 310 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val 330 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly 345 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile 360 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile Asp Gly Thr 390 Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn Met Leu Ser 410 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg Tyr Thr 425 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe 490 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe 505 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr 520 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala

Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg 545 555 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu 600 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu 615 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val 630 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg 665 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met 680 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser 715 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu 745 Leu Arg Arg Gln Lys 755 <210> 42 <211> 5169 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: pHL3258 <220> <221> CDS <222> (191)..(2461) <400> 42 cccaaaaaaa aaaaaaaaa aagagtccag agtggccccg ccgctccgcg ccgggggggg 60 ggggggggg ggacactttc ggacatctgg tcgacctcca gcatcggggg aaaaaaaaa 120 acaaagtgtc geceggagta etggtegace teegaagttg ggggggageg aaageaggea 180 aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro

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							gga Gly								373
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							aca Thr 85								469
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							gtg Val								661
							gac Asp 165								709
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							aaa Lys								901
		_					ggg Gly 245	-							949
							agt Ser								997
(gag Glu								1045

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ccc Pro 510	agc Ser	ttt Phe	ggg ggg	gtg Val	tct Ser 515	ggg Gly	atc Ile	aac Asn	gag Glu	tct Ser 520	gcg Ala	gac Asp	atg Met	agt Ser	att Ile 525	1765
gga Gly	gtt Val	act Thr	gtc Val	atc Ile 530	aaa Lys	aac Asn	aat Asn	atg Met	ata Ile 535	aac Asn	aat Asn	gat Asp	ctt Leu	ggt Gly 540	cca Pro	1813
gca	acc	gct	caa	atg	gcc	ctt	cag	ctg	ttc	atc	aaa	gat	tac	agg	tac	1861

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														tct Ser		2389
														tcc Ser		2437
			ctc Leu					tagt	gaat	itt a	agctt	gtc	ct to	catga	aaaa	2491
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gcc	ggccc	cct d	cctac	gaco	g gg	acac	acga	a ggg	gacco	gaag	gcc	ggcc	agg (cgcga	acctct	2851

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<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pHL3258

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Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln 35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro 50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu 85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu 100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr 115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala 130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser 145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys 165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg 180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg 195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu 210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala 225 230 235 240

Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu 245 250 255

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro 265 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys 280 Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly 300 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala 315 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val 325 330 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly 345 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro 375 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn Met Leu Ser 410 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr 425 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn 455 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys 475 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe 490 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe 505 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala 535 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile 570 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu 600

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu 610 615 620	
Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val 625 630 635 640	
Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu 645 650 655	
Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg 660 670	
Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met 675 680 695	
Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser 690 695 700	
Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser 705 710 715 720	
Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys 725 730 735	•
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acaaagtgto goooggagta otggtogaco toogaagttg ggggggagog aaagcaggoa l	180
	229
gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 2 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro 15 20 25	277
tac age cat ggg aca gga aca gga tac acc atg gat act gtc aac agg Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg 30 35 40 45	325
aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr 50 55 60	373

					aac Asn											421
-		_			gcc Ala			_	_	_	_	_	_	_	_	469
					cat His											517
acg Thr 110	atg Met	gag Glu	gtt Val	gtt Val	cag Gln 115	caa Gln	aca Thr	cga Arg	gtg Val	gac Asp 120	aag Lys	ctg Leu	aca Thr	caa Gln	ggc Gly 125	565
					tgg Trp											613
_	_				ata Ile	_			_					_	_	661
					ctc Leu											709
_			-	-	atg Met							_	_	_	_	757
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					aga Arg											853
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					acc Thr											949
					gca Ala											997
					ggc Gly 275											1045
					acc Thr											1093
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					aca Thr											1189

	aat Asn 335													1237
	ctg Leu													1285
	caa Gln													1333
	gaa Glu													1381
	ggg Gly													1429
	tta Leu 415													1477
	cac His													1525
-	ttt Phe	-	_			_			_				_	1573
	gtc Val													1621
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	ttt Phe 495													1717
_	agc Ser		~ 1	 _	~ 1		_	 		_		~ -		1765
	gta Val													1813
	aca Thr													1861
	tac Tyr		-			-				_				1909
	gag Glu 575													1957

														ctc Leu		2005
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-					-			_		_				gcc Ala		2149
														ccc Pro		2197
														gaa Glu		2245
_					_		_				_			ttc Phe 700		2293
														gag Glu		2341
_	_		_	-	_		_	-	-		-		_	tct Ser	-	2389
														tcc Ser		2437
			ctc Leu					tagt	gaat	itt á	agctt	igte	ct to	catga	aaaa	2491
atgo	ctto	gtt t	tctac	ctaat	a ac	cccg	gegge	c cca	aaaat	gcc	gact	cgga	agc (gaaa	gatata	2551
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tcto	ggtca	aac o	ccag	gaca	ic ac	gcgg	ggago	ago	gcc	gggc	cgg	ggac	gcc (ctcc	caacca	2731
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cggg	geege	cac c	gagag	gctca	ig go	gage	gctct	ccc	gacto	ccgc	acg	ggga	ctc (gcca	gaaagg	2911
atco	gtgad	cct o	gcatt	aato	ga at	cago	gggat	aad	cgcaç	ggaa	agaa	acat	gtg :	agcaa	aaaggc	29-1
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- <210> 45 <211> 757 <212> PRT <213> Art. <223> Desc <400> 45
- <213> Artificial Sequence
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- Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro 50 60
- Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser 65 70 75 80
- Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu 85 95
- Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu 100 105 110
- Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr 115 120 125
- Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala 130 $$135\$
- Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser 145 150 155 160
- Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg 180 185 190
- Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg 195 200 205
- Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu 210 215 220
- Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala 225 230 235 240
- Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu 245 250 255
- Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro 260 265 270
- Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys 275 280 285
- Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly 290 295 300
- Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala 305 310 315 320

Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly 345 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn Met Leu Ser 410 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr 425 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn 455 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala 535 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu 615 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg 660 665

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser 695 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser 715 720 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu 745 Leu Arg Arg Gln Lys 755 <210> 46 <211> 5169 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: pHL3268 <220> <221> CDS <222> (191)..(2461) <400> 46 cccaaaaaaa aaaaaaaaa aagagtccaq agtqqccccq ccqctccqcq ccqgqqqqq 60 ggggggggg ggacactttc ggacatctgg tcgacctcca gcatcggggg aaaaaaaaa 120 acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180 229 aaccatttqa atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro 15 . 325 tac age cat ggg aca gga aca gga tac ace atg gat act gtc aac agg Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr 421 gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn 65 gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469 Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala 85 517 tto ott gag gaa too cat oot ggt ato ttt gag acc tog tgt ott gaa Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu 100 105 acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565

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		gcc Ala														661
.aat Asn		tct Ser 160														709
		aaa Lys														757
_		aga Arg	-		_		_		_			_	-			805 •
		agg Arg	_	_	_	_				_					_	853
		ctg Leu														901
		gca Ala 240														949
		gag Glu														997
		cca Pro														1045
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		gcc Ala 320														1189
_		gtt Val		_		_			-					_		1237
		gga Gly														1285
		ata Ile														1333

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					ttg Leu											1429
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					ctg Leu											1957
					ggc Gly 595											2005
					ctg Leu											2053
					ccc Pro											2101
					gct Ala											2149

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gaa caa atg tac cag aag tgt tgc aac cta ttc gag aaa ttc ttc cct Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro 690 695 700	2293
age age tea tac aga aga cea gtt gga att tee agt atg gtg gag gee Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala 705 710 715	2341
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Leu Arg Arg Gln Lys